



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 07:56 PM UTC

PDB ID : 6VWN / pdb_00006vwn
EMDB ID : EMD-21422
Title : 70S ribosome bound to HIV frameshifting stem-loop (FSS) and P-site tRNA (non-rotated conformation, Structure II)
Authors : Loerch, S.; Bao, C.; Ling, C.; Korostelev, A.A.; Grigorieff, N.; Ermolenko, D.M.
Deposited on : 2020-02-20
Resolution : 3.40 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

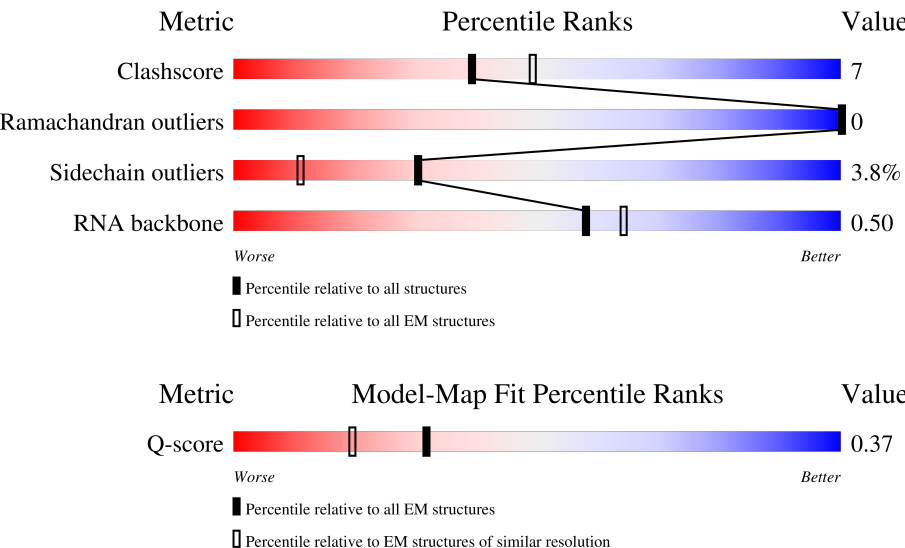
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	3	120	
2	5	76	
3	A	273	

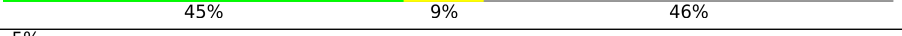
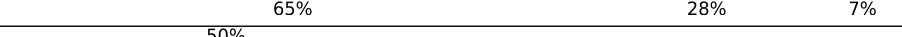
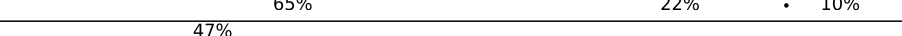
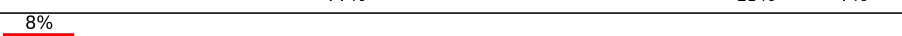
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Mol	Chain	Length	Quality of chain
4	B	209	
5	C	201	
6	D	179	
7	E	177	
8	F	149	
9	G	142	
10	I	123	
11	J	144	
12	K	136	
13	L	127	
14	M	117	
15	N	115	
16	O	118	
17	P	103	
18	Q	110	
19	R	100	
20	S	104	
21	T	94	
22	U	85	
23	V	78	
24	W	63	
25	X	59	
26	Y	57	
27	Z	55	
28	AA	46	

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Mol	Chain	Length	Quality of chain
29	AB	65	
30	AC	38	
31	2	2903	
32	a	241	
33	b	233	
34	c	206	
35	d	167	
36	e	135	
37	f	179	
38	g	130	
39	h	130	
40	i	103	
41	j	129	
42	k	124	
43	l	118	
44	m	101	
45	n	89	
46	o	82	
47	p	84	
48	q	75	
49	r	92	
50	s	87	
51	t	71	
52	1	1540	
53	4	93	

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 140036 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	120	A	U	conflict	GB 984297099

- Molecule 2 is a RNA chain called tRNAPhe.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	76	Total	C	N	O	P	0	0
			1619	723	290	531	75		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	D	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	E	173	Total	C	N	O	S	0	0
			1298	817	238	241	2		

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	48	Total	C	N	O	S	0	0
			368	238	63	66	1		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	143	Total	C	N	O	S	0	0
			1043	649	206	186	2		

- Molecule 12 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 13 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 14 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	114	Total	C	N	O		0	0
			875	542	175	158			

- Molecule 15 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 16 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 17 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 18 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 19 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	90	Total	C	N	O	S	0	0
			714	449	136	128	1		

- Molecule 20 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	S	96	Total	C	N	O	0	0
			735	464	138	133		

- Molecule 21 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	93	Total	C	N	O	S	0
			745	474	136	133	2	0

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U	75	Total	C	N	O	S	0
			575	356	116	102	1	0

- Molecule 23 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	V	77	Total	C	N	O	S	0
			625	388	129	106	2	0

- Molecule 24 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	W	60	Total	C	N	O	S	0
			491	303	96	91	1	0

- Molecule 25 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	X	58	Total	C	N	O	S	0
			449	281	87	79	2	0

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	Y	55	Total	C	N	O	S	0
			434	263	92	78	1	0

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	Z	48	Total	C	N	O	0	0
			396	255	72	69		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AA	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AB	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AC	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 31 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	2	2833	Total	C	N	O	P	0	0
			60819	27131	11192	19664	2832		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	208	C	-	insertion	GB 984297099
2	284	U	C	conflict	GB 984297099
2	285	G	A	conflict	GB 984297099
2	356	G	A	conflict	GB 984297099
2	542	C	U	conflict	GB 984297099
2	747	C	U	conflict	GB 984297099
2	1174	U	G	conflict	GB 984297099
2	1211	C	U	conflict	GB 984297099
2	1513	U	C	conflict	GB 984297099
2	1723	G	A	conflict	GB 984297099
2	1730	C	U	conflict	GB 984297099
2	1865	U	C	conflict	GB 984297099
2	2163	A	G	conflict	GB 984297099

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Chain	Residue	Modelled	Actual	Comment	Reference
2	2712	C	U	conflict	GB 984297099
2	2794	C	U	conflict	GB 984297099
2	2796	U	C	conflict	GB 984297099
2	2797	U	C	conflict	GB 984297099
2	2799	A	G	conflict	GB 984297099
2	2802	G	A	conflict	GB 984297099

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	220	Total	C	N	O	S	0	0
			1672	1062	293	310	7		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	197	Total	C	N	O	S	0	0
			1502	957	276	266	3		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	159	Total	C	N	O	S	0	0
			1273	796	240	234	3		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	157	Total	C	N	O	S	0	0
			1146	714	215	211	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	101	Total	C	N	O	S	0	0
			824	520	149	149	6		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	97	Total	C	N	O	S	0	0
			742	467	133	139	3		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	121	Total	C	N	O	S	0	0
			950	591	189	168	2		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	89	Total	C	N	O	S	0	0
			726	455	141	129	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	111	Total	C	N	O	S	0	0
			867	535	180	148	4		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	111	Total	C	N	O	S	0	0
			859	531	172	153	3		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	87	Total	C	N	O	S	0	0
			702	433	140	128	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	78	Total	C	N	O	S	0	0
			632	400	118	111	3		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	q	54	Total	C	N	O	0	0
			443	281	81	81		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	84	Total	C	N	O	S	0	0
			655	406	136	110	3		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	68	Total	C	N	O	S	0	0
			566	351	120	94	1		

- Molecule 52 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	1	1508	Total	C	N	O	P	0	0
			32365	14434	5945	10478	1508		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	1517	A	G	conflict	GB 1726036237

- Molecule 53 is a RNA chain called HIV1 frameshift stimulating sequence mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	4	43	Total	C	N	O	P	0	0
			926	413	174	296	43		

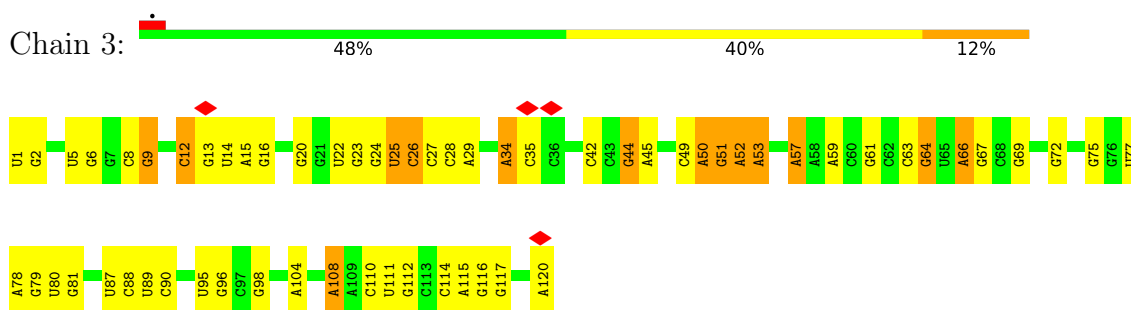
- Molecule 54 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
54	A	2	Total	Mg	0
			2	2	
54	Y	1	Total	Mg	0
			1	1	
54	2	45	Total	Mg	0
			45	45	
54	1	7	Total	Mg	0
			7	7	

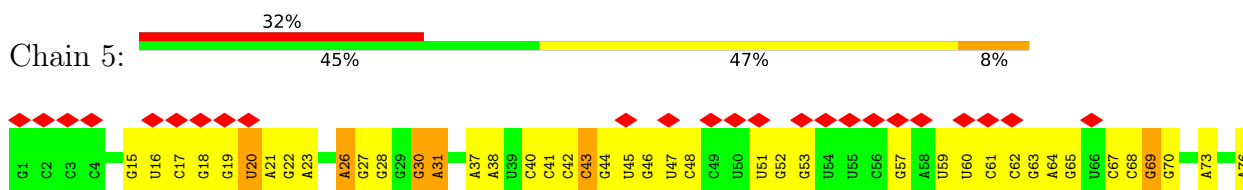
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

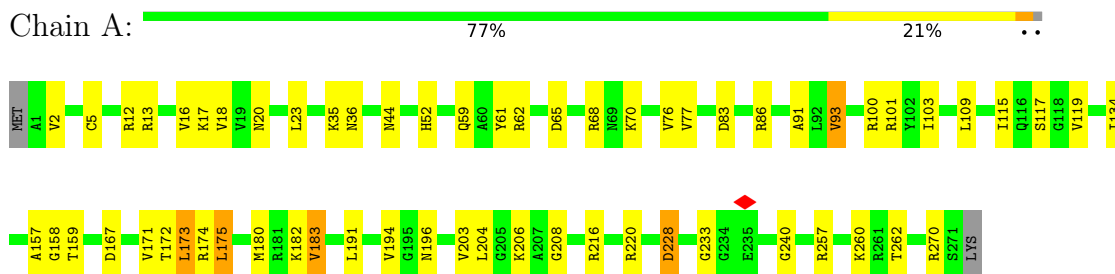
- Molecule 1: 5S ribosomal RNA



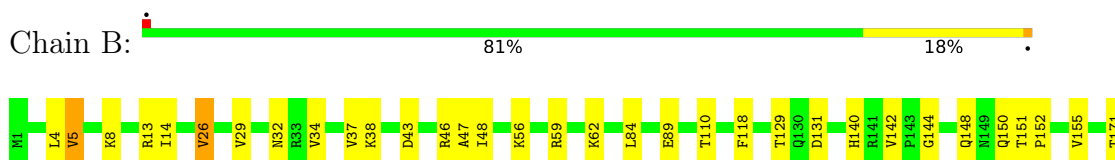
- Molecule 2: tRNA^{Phe}



- Molecule 3: 50S ribosomal protein L2

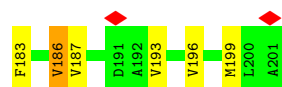
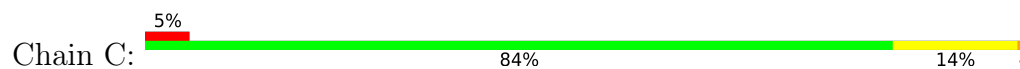


- Molecule 4: 50S ribosomal protein L3

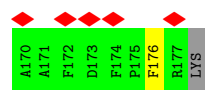
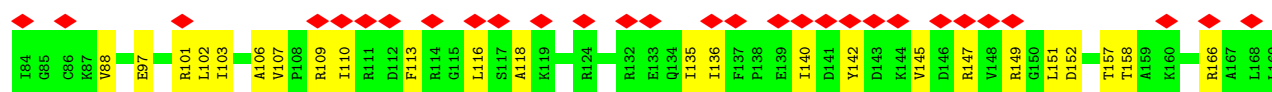
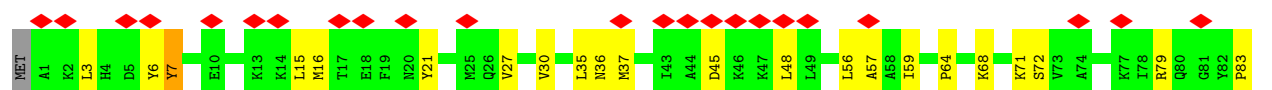




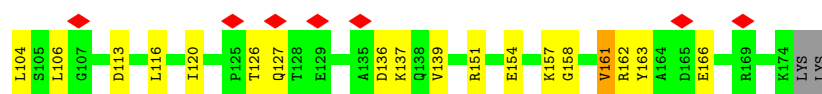
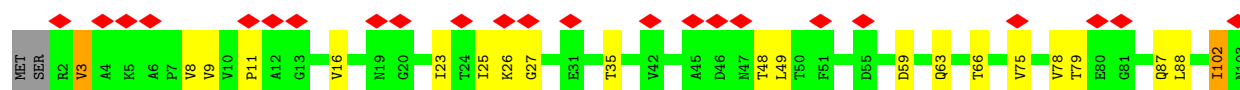
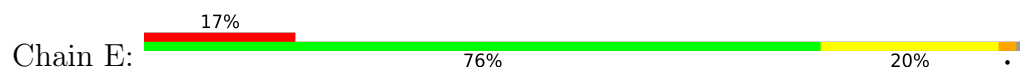
- Molecule 5: 50S ribosomal protein L4



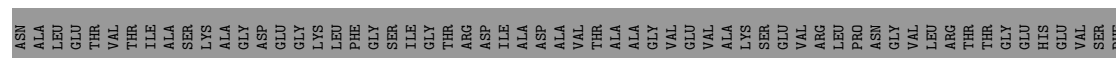
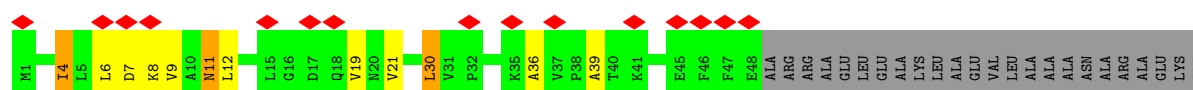
- Molecule 6: 50S ribosomal protein L5



- Molecule 7: 50S ribosomal protein L6



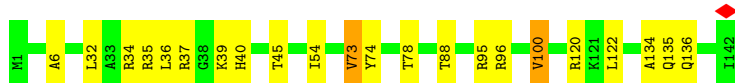
- Molecule 8: 50S ribosomal protein L9



GLN
VAL
HIS
SER
GLU
VAL
PHE
ALA
LYS
VAL
ILE
VAL
ASN
VAL
VAL
ALA
GLU

• Molecule 9: 50S ribosomal protein L13

Chain G:  85% 14%



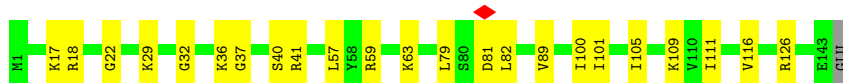
• Molecule 10: 50S ribosomal protein L14

Chain I:  76% 24%



• Molecule 11: 50S ribosomal protein L15

Chain J:  83% 16%



• Molecule 12: 50S ribosomal protein L16

Chain K:  79% 21%



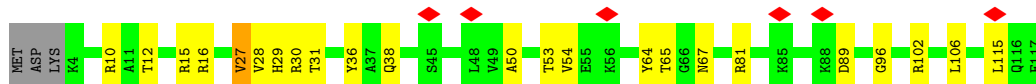
• Molecule 13: 50S ribosomal protein L17

Chain L:  77% 16% 6%



• Molecule 14: 50S ribosomal protein L18

Chain M:  5% 78% 19%



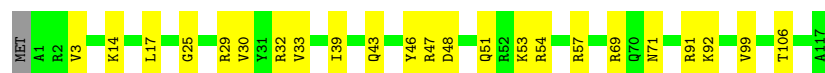
• Molecule 15: 50S ribosomal protein L19

Chain N:  67% 29%



- Molecule 16: 50S ribosomal protein L20

Chain O: 80% 19%



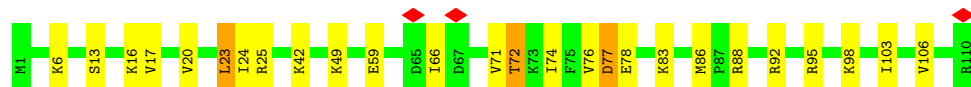
- Molecule 17: 50S ribosomal protein L21

Chain P: 5% 82% 18%



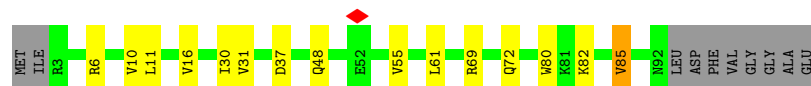
- Molecule 18: 50S ribosomal protein L22

Chain Q: 76% 21%



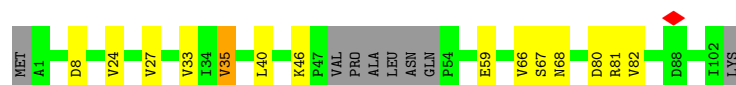
- Molecule 19: 50S ribosomal protein L23

Chain R: 75% 14% 10%



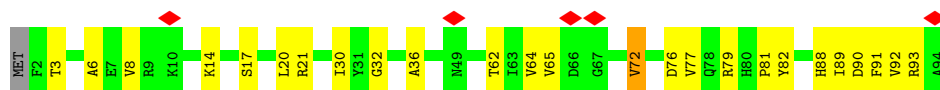
- Molecule 20: 50S ribosomal protein L24

Chain S: 79% 12% 8%

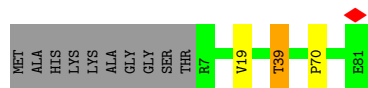
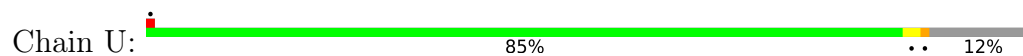


- Molecule 21: 50S ribosomal protein L25

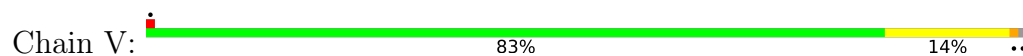
Chain T: 5% 72% 26%



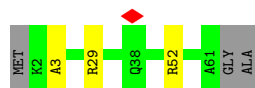
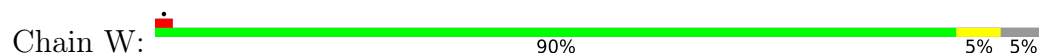
- Molecule 22: 50S ribosomal protein L27



- Molecule 23: 50S ribosomal protein L28



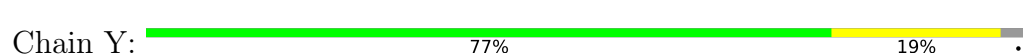
- Molecule 24: 50S ribosomal protein L29



- Molecule 25: 50S ribosomal protein L30



- Molecule 26: 50S ribosomal protein L32



- Molecule 27: 50S ribosomal protein L33



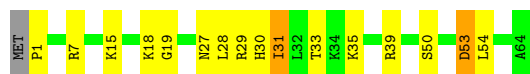
- Molecule 28: 50S ribosomal protein L34

Chain AA:  83% 17%



- Molecule 29: 50S ribosomal protein L35

Chain AB:  74% 22% . .



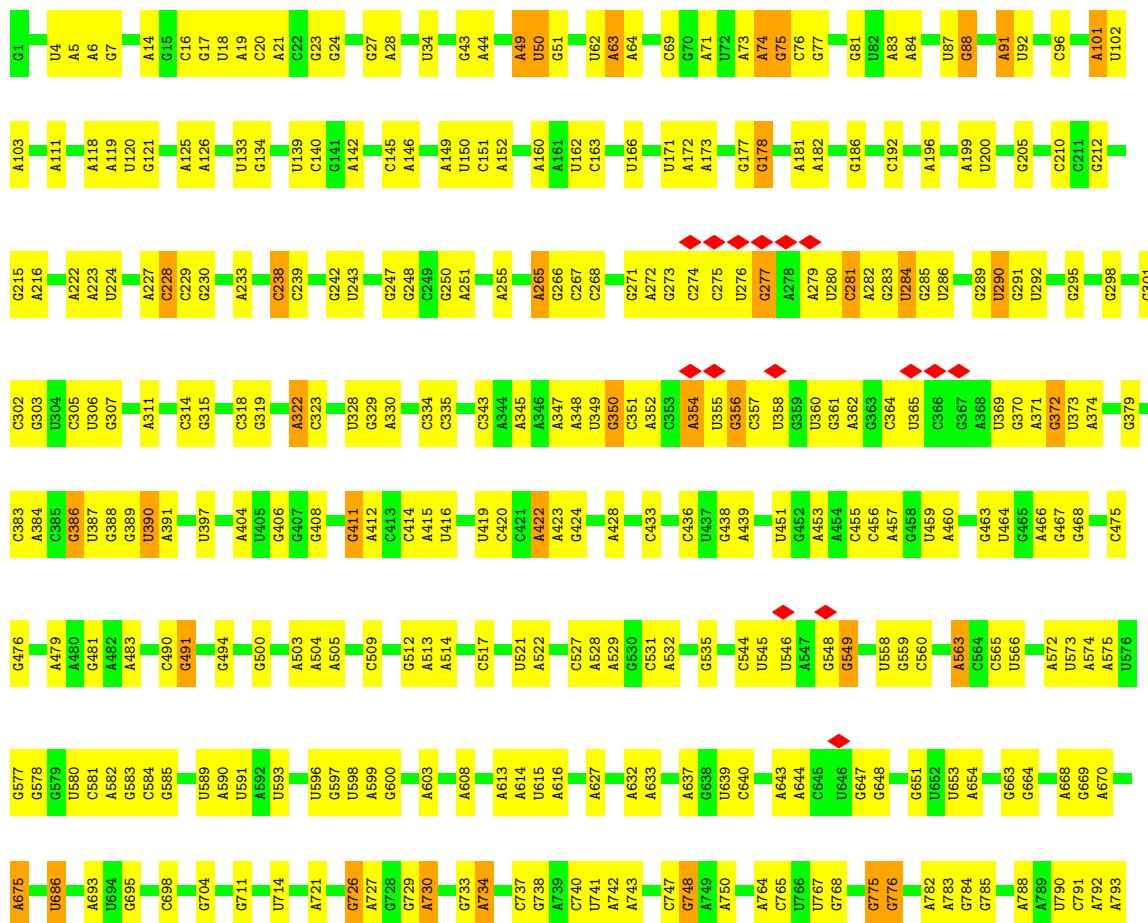
- Molecule 30: 50S ribosomal protein L36

Chain AC:  66% 32% .

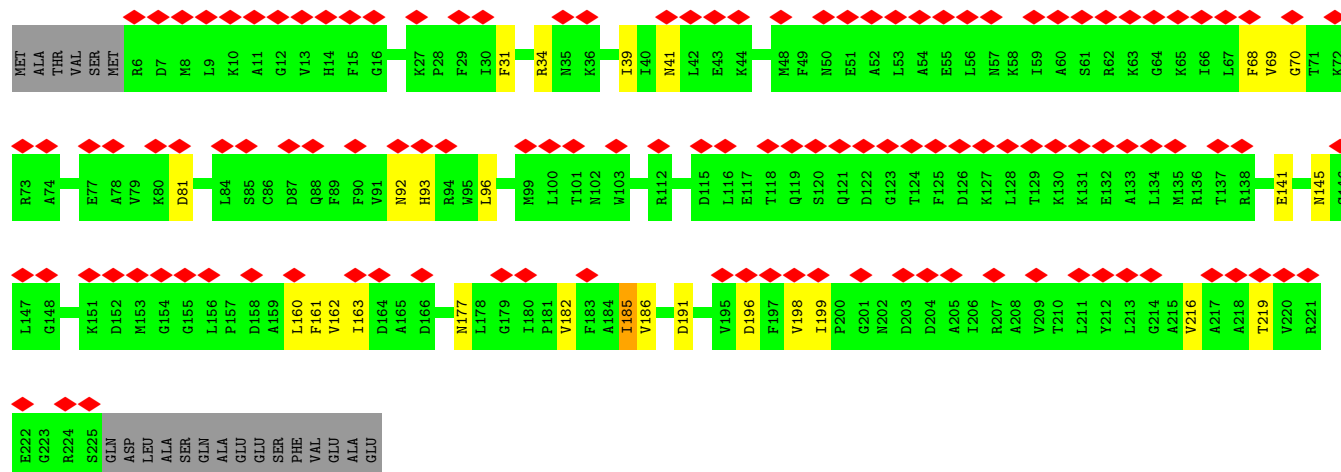
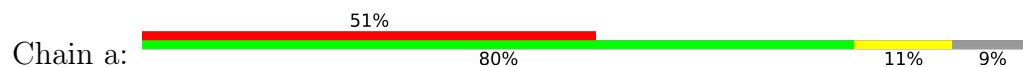
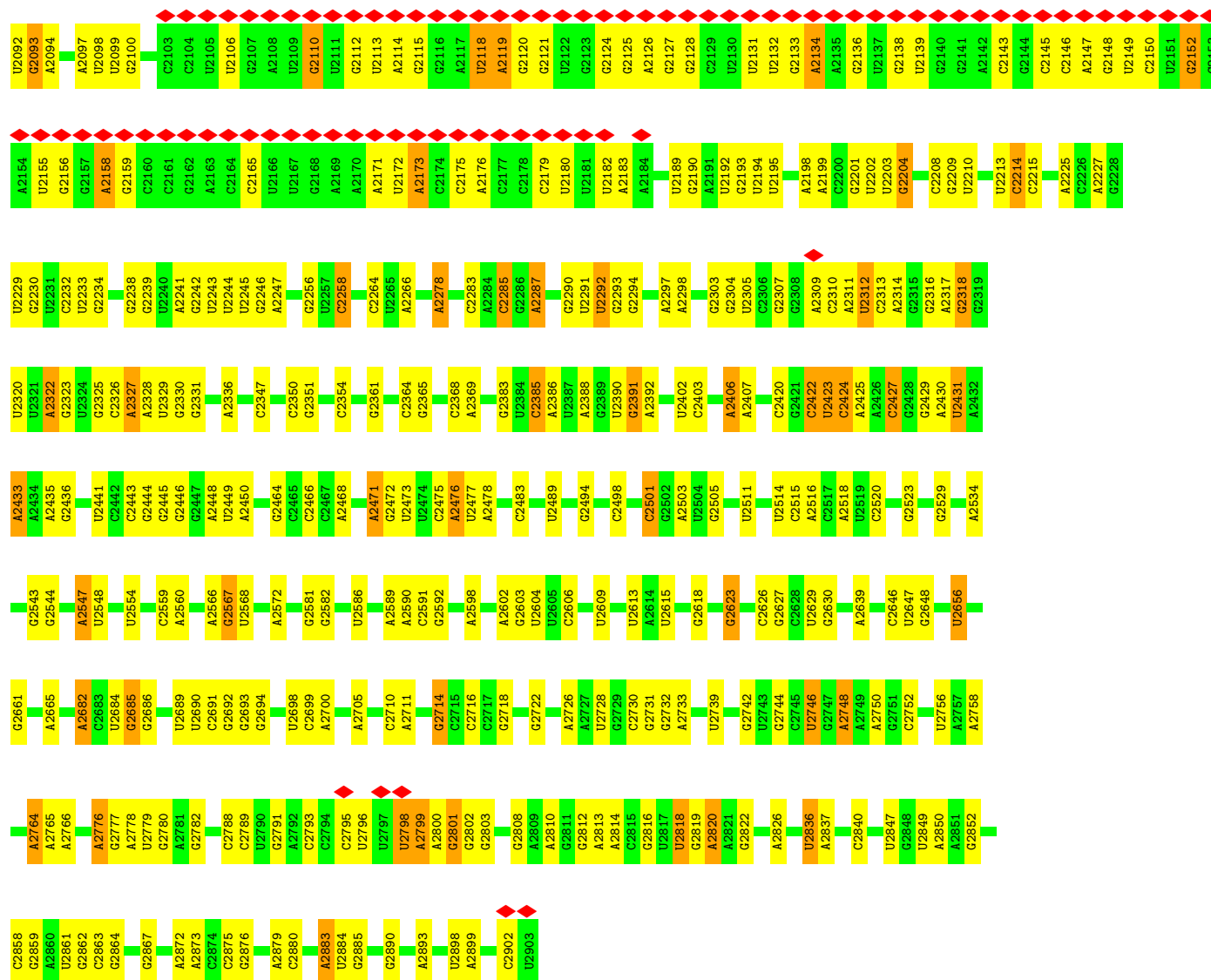


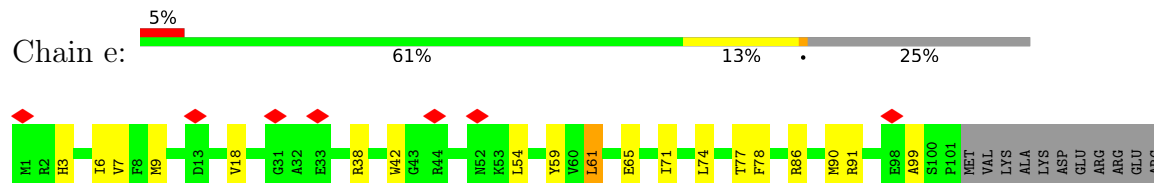
- Molecule 31: 23S ribosomal RNA

Chain 2:  6% 58% 35% 5% .

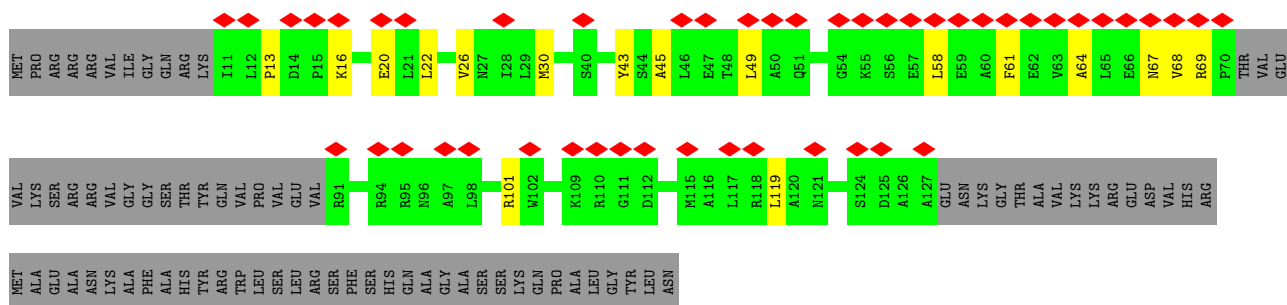


C1990	A1876	G1789	G1695	G1587	C1498	G1421	C1306	C1211	G	U1113	C	A973	C888	A802
U1991	A1877	C1790	G1699	G1588	C1499	A1427	A1307	G1212		G1115	C	G974	C889	G805
U1992	G1878	A1791		A1570	G1500	C1428	G1311				A	A975	C890	U807
U1993	U1880		G1702	A1571	G1501		U1312	U1217		U1119	G	A979	G891	G808
U1995	G1883	C1795	U1709	A1572	A1502	A1431	U1313	G1218			A	A980	A992	G809
C1996	U1796	U1796	G1710	A1573	A1503	G1432	U1316	U1219		G1122	U	A983	A993	U811
C1997	U1884	G1797	G1711	A1574	A1504	A1433	G1317	G1220		G1123	G	A984	U894	C812
	U1885	U1798		A1575	A1505	A1434	C1323	G1223		G1124	U	C985	U895	U813
G2010	A1889	G1799	U1714	A1583	U1506	G1436	U1329	G1225		G1129	C	C986	A996	C814
U2011	A1890	A1801	G1715	U1584	C1507	C1437	U1340	G1226		U1130	U	C987	C997	
G2012	A1893	A1802	G1716	U1584	C1507	U1438	U1341			G1131	U		A899	A819
		A1803	A1717	C1585	A1508	A1439	G1333	U1242		U1132	A	C992	A902	U827
U2022					A1509	U1440	G1334	U1243		U1133	A	G993	U902	U828
C2023	C1902	G1807	G1721	C1592	A1510	U1441	C1335			A1134	G	C994	C903	
G2024		A1808	U1722	G1593	G1511	U1442	A1336	A1247		C1135	A	C995	G904	
C2025	G1906	A1809	G1723	U1594	G1512	G1443		G1248			A	A996	A905	U832
		A1810	G1724	U1513	U1513	G1444	U1340	U1249			C	G997	A906	A833
A2031	C1909	C1816	U1725	G1514	A1515	G1445	U1341	G1250		U1141	C	C998	A907	A834
G2032	G1910	A1817	C1726	A1516	G1516	C1446	G1345	G1251		A1142	A	U999	A910	G835
A2033	U1911	U1817	G1727	G1517	G1517	G1447	C1346	G1252		A1143	G	A1000	A911	C836
U2034	A1912	U1818	C1727	C1518	G1518	U1448		A1253			C	A1009	G914	G837
G2035	A1913	A1819		G1519	A1522	G1452	A1363	A1254		U1148	A	A1010	C915	
C2036					U1523	A1453	A1364	U1255		G1149	A	U1011	C916	U846
A2037	G1924	G1826	U1729	A1614	U1524	C1454	A1365	G1256		C1150	U	U1012	A918	U847
G2038	C1925	A1829	C1730	G1615	G1525	G1455					C	A1013	A919	C848
U2039	U1926	G1830	G1731	C1616	G1526	U1456	G1360	C1257		C1153	A	A1014	G923	A849
G2040	A1927	C1831	G1732	U1636	A1526	G1457	C1361	U1258		G1154	U			U850
	U1928	G1831	G1733	C1637	C1527		C1362	G1259		A1155	U	A1020	G926	C851
C2043	G1929	G1835	U1734	C1638	G1528		G1363	A1264		C1161	A	A1021	A927	U852
	U1930		C1735	C1639	A1528		G1364	A1265		G1162	A	G1022	A928	
C2047	A1936	G1839	U1736	C1646	G1529	U1460	A1367	G1266		G1163	A			G857
G2048	A1937	C1845	G1737	U1647	G1530	C1461	G1368			A1164	A	G1026	U831	G858
A2052	U1938	G1845	U1738	U1648	C1531	U1466	G1369	C1270		G1165	A	A1027	U832	U860
	A1939				A1532	A1469		G1271			A	A1028	A933	
C2055	U1940	A1848	A1744	A1652	C1533	G1475	A1378	A1272		G1168	A	C1030	U934	A863
G2056	C1942	G1849	A1745	G1653	U1534	U1476	U1379			A1169	A	G1031	A936	C864
A2060		U1851	A1746	A1654	U1535	A1477		A1275		G1170	C	A1032		G865
G2061	G1954	C1852	U1747		C1536	G1478	C1386	C1278		U1172	U	U1033	A941	A866
A2062	U1955	A1853		G1663	U1537		A1387	G1279		U1173	A			G869
	U1956		C1752	G1667	G1538	U1481	G1388			U1174	A	G1036	A945	
G2069		U1856	G1753	A1668	U1539	G1482		G1283		A1175	U	G1037	C946	C873
A2070	A1960	G1857	A1754	C1669	U1540	G1483	A1395			U1176	G	A1039	G950	G874
A2071	G1964	U1858	G1755	A1689	C1541	U1484		A1286		U1177	C	A1040		G875
C2072		G1859	U1756	C1670	G1542	U1485	G1407	A1287		G1178	U	G1041	G953	A878
G2073		G1860			U1544	U1486	G1408	G1288		U1179	C	G1042	G954	G879
U2074	C1967		A1759	G1674	A1545	U1487	U1409	C1289		U1180	A	C	C957	G880
U2075		U1864			A1546	U1488	U1410	C1291		G1186	U	C		G881
	A1970	U1865	A1762	G1681	A1547	U1489	G1411	U1292			G	C	A961	G882
U2081	U1971	A1866	G1763	G1682	A1548	U1490	G1416			G1190	A	G	U963	G883
A2082	G1972	G1867	C1764	U1683	G1549	U1491		A1301		U1198	U	A	A967	U884
		C1868		G1684	C1547	G1492	A1419	G1303		U1199	C	C	U967	C885
G1983		G1869	A1773	G1689	A1548	A1493	A1420				G	A	G968	A886
		A1870		A1690	U1554	A1494					U	A	C969	
A1987		A1871	U1782	U1693	U1559	C1495					C	A	U970	U887
G1988		A1872	A1783	G1694	G1560	A1496					G	A		
G1989			A1784	C1694	U1562	A1497					A			
				C1565	U1563									
				C1566										

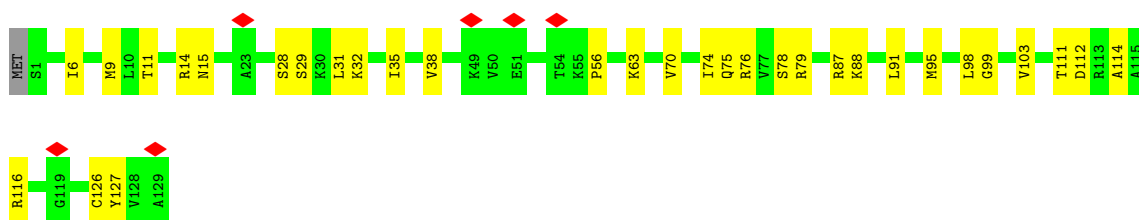




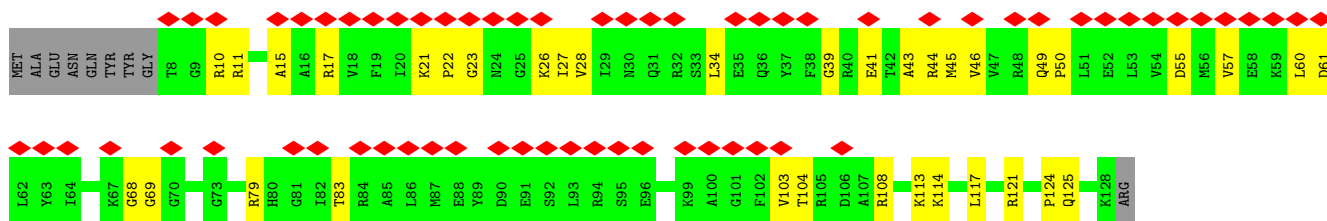
Chain f:



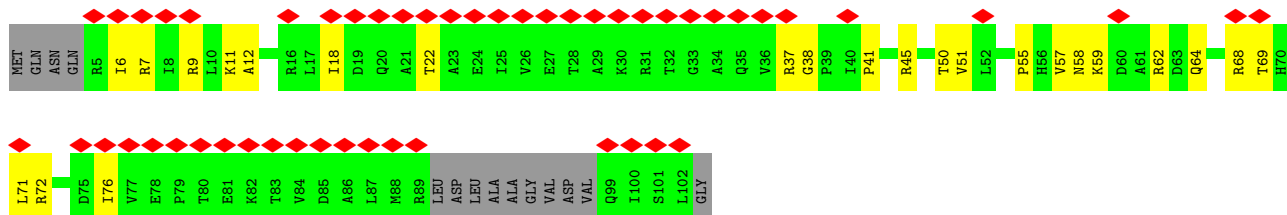
Chain g:



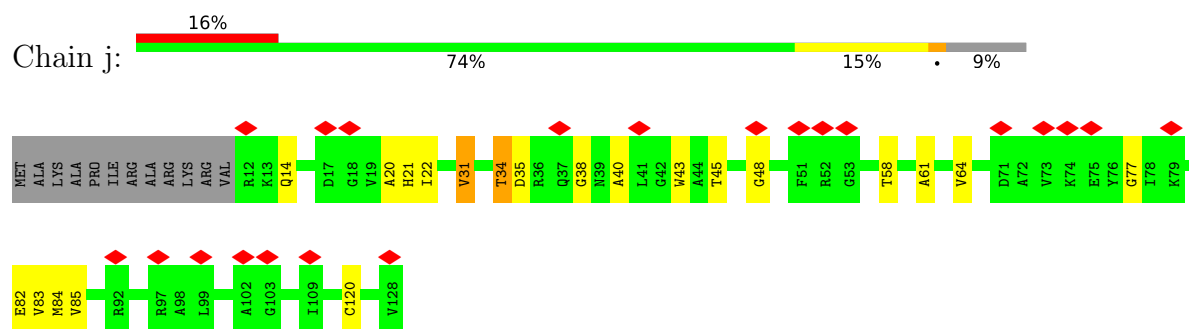
Chain h:



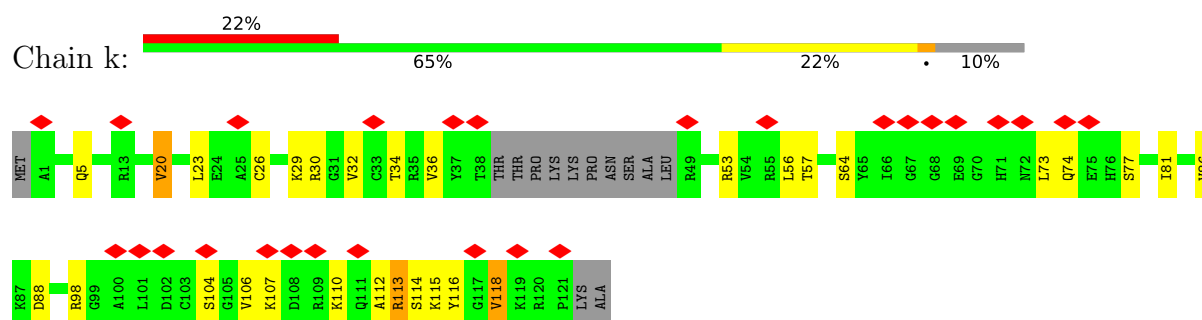
Chain i:



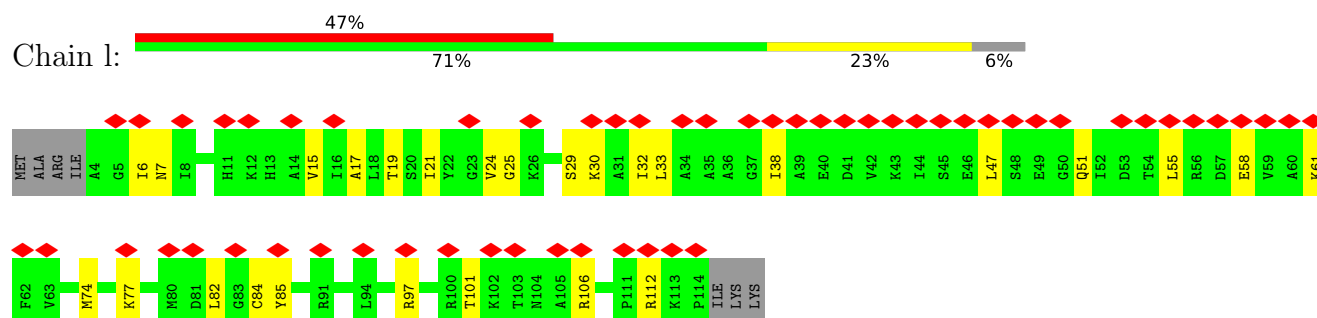
- Molecule 41: 30S ribosomal protein S11



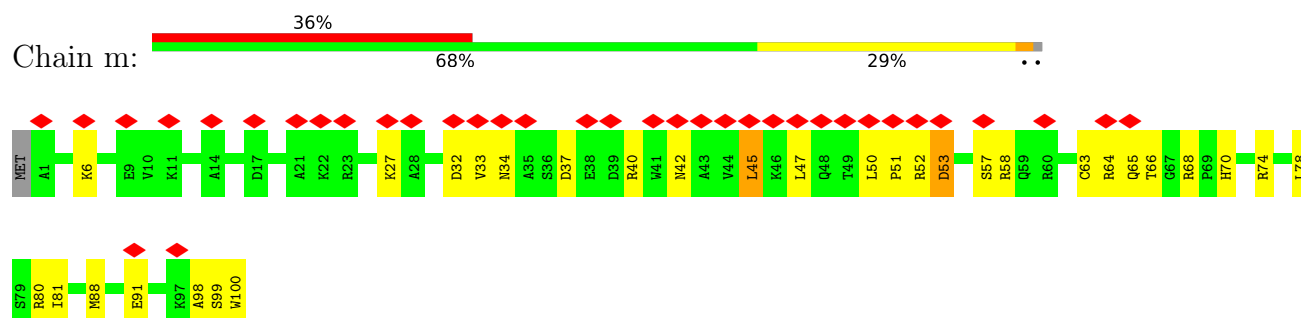
- Molecule 42: 30S ribosomal protein S12



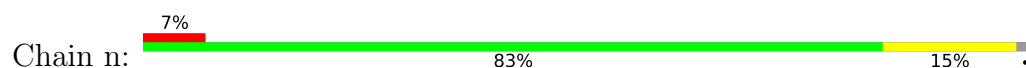
- Molecule 43: 30S ribosomal protein S13



- Molecule 44: 30S ribosomal protein S14

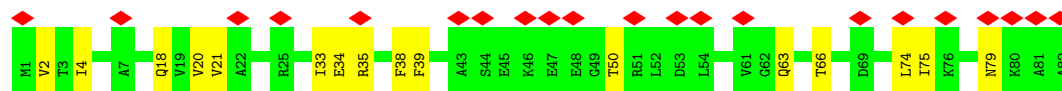
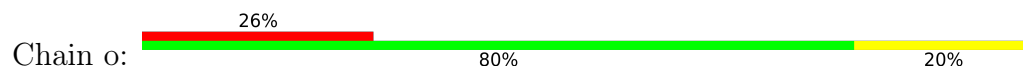


- Molecule 45: 30S ribosomal protein S15

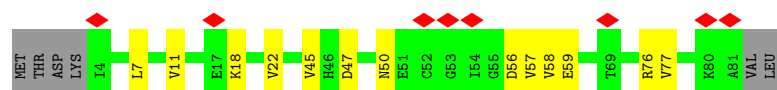
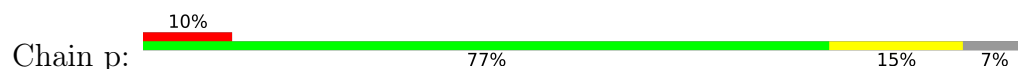




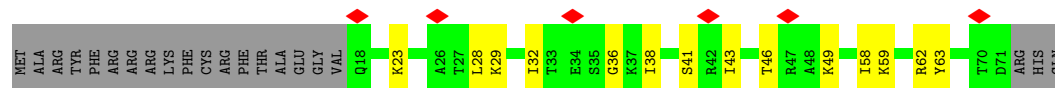
- Molecule 46: 30S ribosomal protein S16



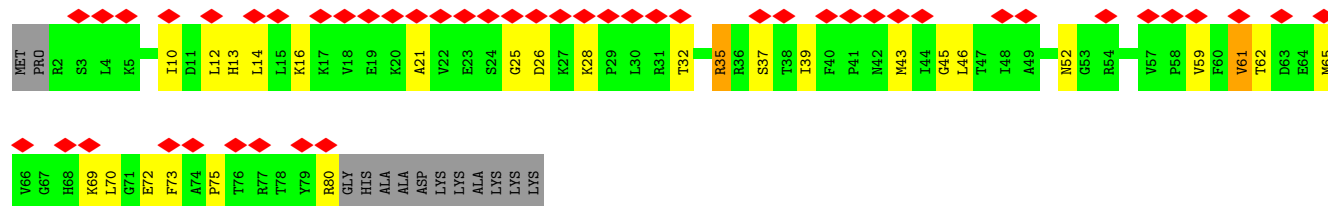
- Molecule 47: 30S ribosomal protein S17



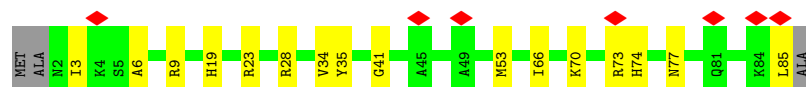
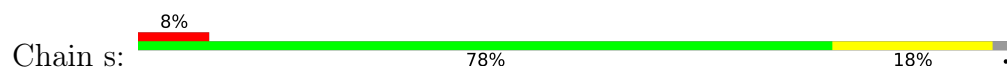
- Molecule 48: 30S ribosomal protein S18



- Molecule 49: 30S ribosomal protein S19

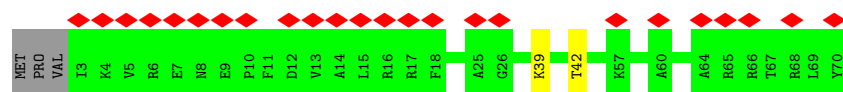


- Molecule 50: 30S ribosomal protein S20

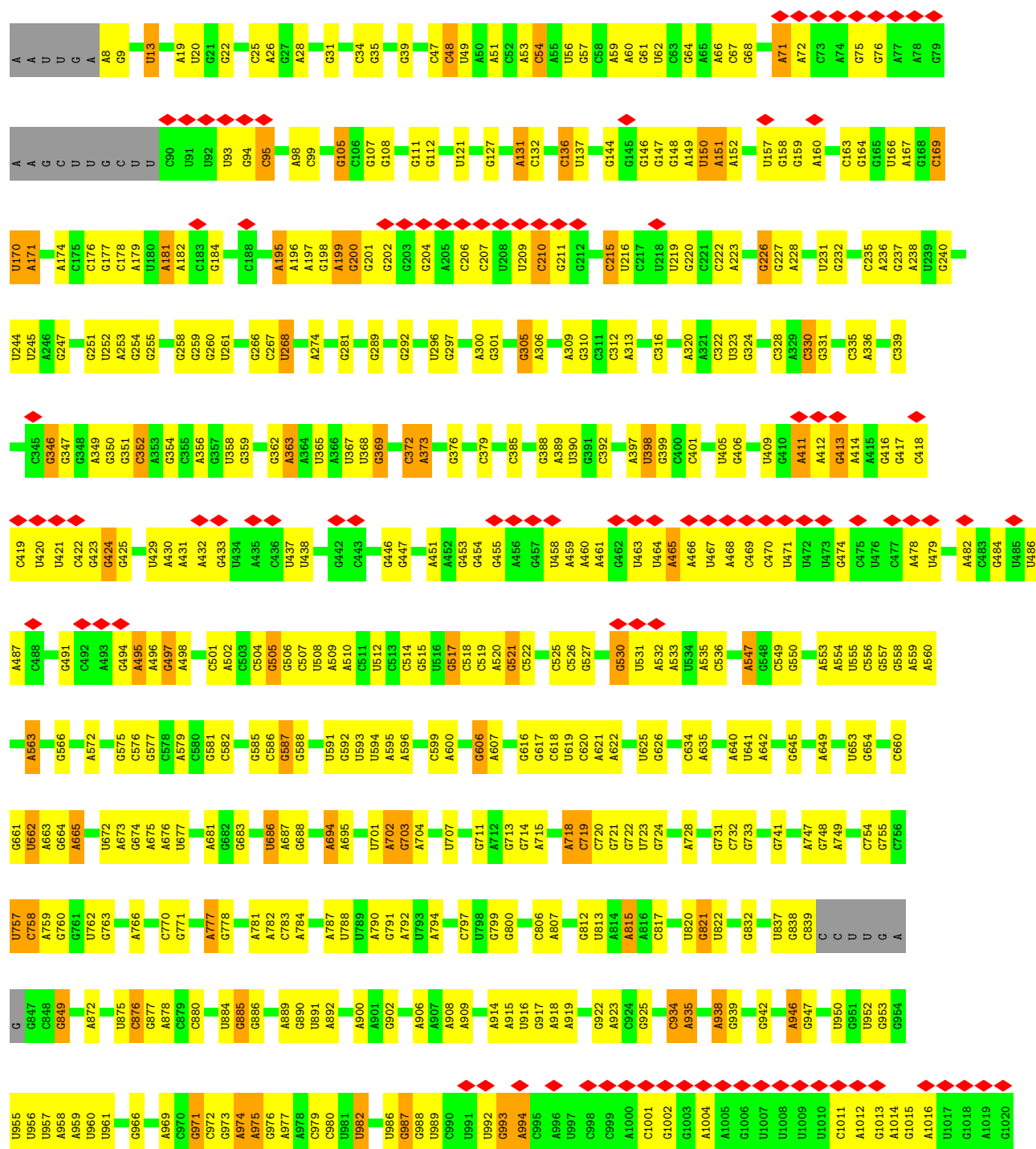


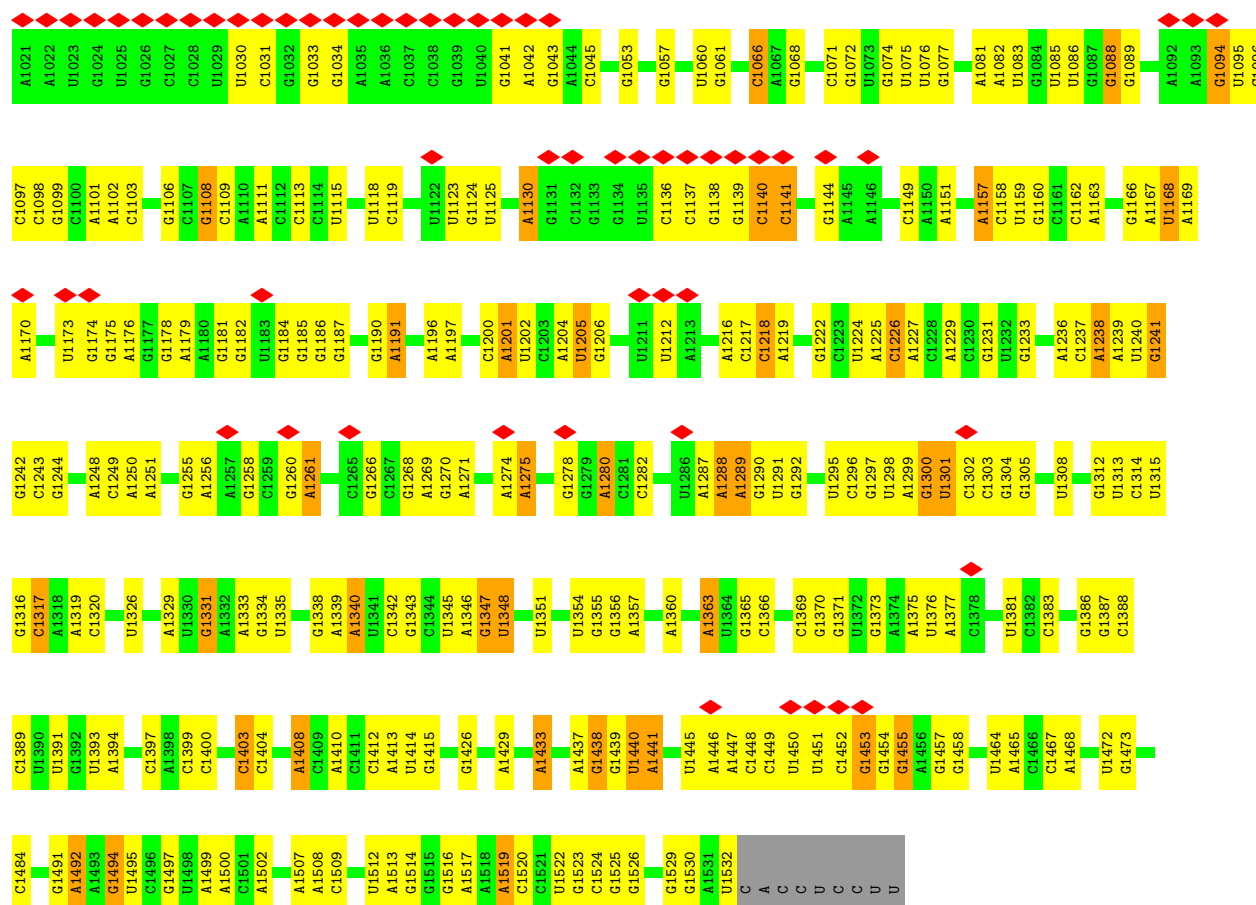
- Molecule 51: 30S ribosomal protein S21



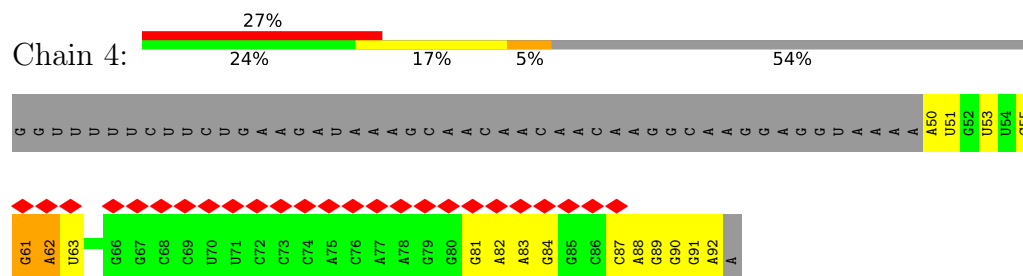


• Molecule 52: 16S ribosomal RNA





• Molecule 53: HIV1 frameshift stimulating sequence mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	640261	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	27.710	Depositor
Minimum map value	-8.896	Depositor
Average map value	0.203	Depositor
Map value standard deviation	1.100	Depositor
Recommended contour level	5.8	Depositor
Map size ($\text{\AA}$)	654.48, 654.48, 654.48	wwPDB
Map dimensions	648, 648, 648	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.01, 1.01, 1.01	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	3	0.12	0/2872	0.27	0/4479
2	5	0.13	0/1809	0.31	0/2819
3	A	0.13	0/2121	0.33	0/2852
4	B	0.12	0/1586	0.33	0/2134
5	C	0.12	0/1571	0.31	0/2113
6	D	0.14	0/1434	0.40	0/1926
7	E	0.12	0/1318	0.33	0/1786
8	F	0.13	0/373	0.40	0/502
9	G	0.12	0/1152	0.31	0/1551
10	I	0.12	0/956	0.34	0/1279
11	J	0.11	0/1052	0.31	0/1401
12	K	0.12	0/1093	0.33	0/1460
13	L	0.17	0/964	0.41	0/1289
14	M	0.13	0/885	0.38	0/1187
15	N	0.12	0/929	0.36	0/1242
16	O	0.14	0/960	0.32	0/1278
17	P	0.14	0/829	0.38	0/1107
18	Q	0.12	0/864	0.35	0/1156
19	R	0.11	0/720	0.32	0/962
20	S	0.11	0/741	0.30	0/984
21	T	0.12	0/758	0.36	0/1015
22	U	0.12	0/582	0.34	0/769
23	V	0.13	0/635	0.35	0/848
24	W	0.12	0/492	0.31	0/655
25	X	0.13	0/453	0.31	0/605
26	Y	0.12	0/440	0.33	0/588
27	Z	0.10	0/403	0.29	0/538
28	AA	0.12	0/380	0.35	0/498
29	AB	0.14	0/513	0.34	0/676
30	AC	0.14	0/303	0.35	0/397
31	2	0.12	0/68117	0.27	0/106268
32	a	0.12	0/1703	0.35	0/2305

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.15	0/1528	0.35	0/2069
34	c	0.14	0/1289	0.41	0/1729
35	d	0.14	0/1159	0.38	0/1561
36	e	0.14	0/843	0.40	0/1140
37	f	0.15	0/750	0.41	0/1009
38	g	0.11	0/989	0.33	0/1326
39	h	0.22	0/960	0.46	0/1280
40	i	0.14	0/735	0.38	0/991
41	j	0.13	0/893	0.40	0/1205
42	k	0.17	0/878	0.46	0/1176
43	l	0.13	0/868	0.37	0/1161
44	m	0.13	0/817	0.37	0/1088
45	n	0.13	0/710	0.32	0/950
46	o	0.14	0/659	0.35	0/884
47	p	0.13	0/641	0.37	0/860
48	q	0.12	0/449	0.36	0/604
49	r	0.20	0/652	0.44	0/877
50	s	0.14	0/661	0.32	0/876
51	t	0.13	0/573	0.34	0/759
52	1	0.12	0/36240	0.28	0/56532
53	4	0.15	0/1037	0.28	0/1616
All	All	0.13	0/152339	0.30	0/228362

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3	2568	0	1303	37	0
2	5	1619	0	822	25	0
3	A	2082	0	2157	41	0
4	B	1565	0	1616	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	1552	0	1619	19	0
6	D	1410	0	1447	23	0
7	E	1298	0	1340	23	0
8	F	368	0	387	7	0
9	G	1129	0	1162	14	0
10	I	947	0	1023	17	0
11	J	1043	0	1123	17	0
12	K	1074	0	1157	19	0
13	L	951	0	994	12	0
14	M	875	0	906	11	0
15	N	917	0	965	25	0
16	O	947	0	1022	16	0
17	P	816	0	839	13	0
18	Q	857	0	922	20	0
19	R	714	0	773	6	0
20	S	735	0	788	10	0
21	T	745	0	768	15	0
22	U	575	0	592	2	0
23	V	625	0	655	9	0
24	W	491	0	523	2	0
25	X	449	0	491	9	0
26	Y	434	0	448	6	0
27	Z	396	0	424	9	0
28	AA	377	0	418	6	0
29	AB	504	0	574	11	0
30	AC	302	0	343	11	0
31	2	60819	0	30591	587	0
32	a	1672	0	1649	15	0
33	b	1502	0	1534	31	0
34	c	1273	0	1304	23	0
35	d	1146	0	1184	19	0
36	e	824	0	815	11	0
37	f	742	0	762	11	0
38	g	979	0	1034	22	0
39	h	950	0	993	23	0
40	i	726	0	766	21	0
41	j	877	0	887	14	0
42	k	867	0	917	24	0
43	l	859	0	912	21	0
44	m	805	0	847	25	0
45	n	702	0	724	6	0
46	o	649	0	666	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	p	632	0	669	5	0
48	q	443	0	466	10	0
49	r	637	0	665	21	0
50	s	655	0	705	12	0
51	t	566	0	597	1	0
52	1	32365	0	16288	466	0
53	4	926	0	467	20	0
54	1	7	0	0	0	0
54	2	45	0	0	0	0
54	A	2	0	0	0	0
54	Y	1	0	0	0	0
All	All	140036	0	93043	1621	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 1621 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:1:412:A:H62	52:1:431:A:N6	1.36	1.24
53:4:62:A:N6	53:4:91:G:H1	1.47	1.11
52:1:412:A:N6	52:1:431:A:H61	1.52	1.08
31:2:2114:A:C6	31:2:2119:A:N6	2.26	1.02
31:2:1527:G:H21	31:2:1545:A:N6	1.59	1.01

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	A	269/273 (98%)	260 (97%)	9 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	B	207/209 (99%)	202 (98%)	5 (2%)	0	100	100
5	C	199/201 (99%)	192 (96%)	7 (4%)	0	100	100
6	D	175/179 (98%)	167 (95%)	8 (5%)	0	100	100
7	E	171/177 (97%)	160 (94%)	11 (6%)	0	100	100
8	F	46/149 (31%)	39 (85%)	7 (15%)	0	100	100
9	G	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
10	I	121/123 (98%)	119 (98%)	2 (2%)	0	100	100
11	J	141/144 (98%)	136 (96%)	5 (4%)	0	100	100
12	K	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
13	L	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
14	M	112/117 (96%)	106 (95%)	6 (5%)	0	100	100
15	N	112/115 (97%)	103 (92%)	9 (8%)	0	100	100
16	O	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
17	P	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
18	Q	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
19	R	88/100 (88%)	86 (98%)	2 (2%)	0	100	100
20	S	92/104 (88%)	92 (100%)	0	0	100	100
21	T	91/94 (97%)	87 (96%)	4 (4%)	0	100	100
22	U	73/85 (86%)	73 (100%)	0	0	100	100
23	V	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
24	W	58/63 (92%)	58 (100%)	0	0	100	100
25	X	56/59 (95%)	56 (100%)	0	0	100	100
26	Y	53/57 (93%)	53 (100%)	0	0	100	100
27	Z	46/55 (84%)	45 (98%)	1 (2%)	0	100	100
28	AA	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
29	AB	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
30	AC	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
32	a	218/241 (90%)	208 (95%)	10 (5%)	0	100	100
33	b	193/233 (83%)	188 (97%)	5 (3%)	0	100	100
34	c	157/206 (76%)	148 (94%)	9 (6%)	0	100	100
35	d	155/167 (93%)	152 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	e	99/135 (73%)	90 (91%)	9 (9%)	0	100	100
37	f	93/179 (52%)	86 (92%)	7 (8%)	0	100	100
38	g	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
39	h	119/130 (92%)	104 (87%)	15 (13%)	0	100	100
40	i	85/103 (82%)	80 (94%)	5 (6%)	0	100	100
41	j	115/129 (89%)	105 (91%)	10 (9%)	0	100	100
42	k	107/124 (86%)	93 (87%)	14 (13%)	0	100	100
43	l	109/118 (92%)	101 (93%)	8 (7%)	0	100	100
44	m	98/101 (97%)	93 (95%)	5 (5%)	0	100	100
45	n	85/89 (96%)	84 (99%)	1 (1%)	0	100	100
46	o	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
47	p	76/84 (90%)	67 (88%)	9 (12%)	0	100	100
48	q	52/75 (69%)	50 (96%)	2 (4%)	0	100	100
49	r	77/92 (84%)	69 (90%)	8 (10%)	0	100	100
50	s	82/87 (94%)	80 (98%)	2 (2%)	0	100	100
51	t	66/71 (93%)	65 (98%)	1 (2%)	0	100	100
All	All	5235/5843 (90%)	5008 (96%)	227 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	A	216/218 (99%)	205 (95%)	11 (5%)	21	48
4	B	164/164 (100%)	158 (96%)	6 (4%)	30	55
5	C	165/165 (100%)	161 (98%)	4 (2%)	43	62
6	D	148/150 (99%)	142 (96%)	6 (4%)	27	52
7	E	134/138 (97%)	128 (96%)	6 (4%)	24	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	F	39/114 (34%)	35 (90%)	4 (10%)	7	24
9	G	116/116 (100%)	113 (97%)	3 (3%)	40	61
10	I	104/104 (100%)	100 (96%)	4 (4%)	29	54
11	J	102/103 (99%)	99 (97%)	3 (3%)	37	60
12	K	109/109 (100%)	107 (98%)	2 (2%)	51	67
13	L	99/103 (96%)	98 (99%)	1 (1%)	68	75
14	M	84/87 (97%)	79 (94%)	5 (6%)	17	43
15	N	99/100 (99%)	90 (91%)	9 (9%)	9	30
16	O	89/90 (99%)	86 (97%)	3 (3%)	32	57
17	P	84/84 (100%)	82 (98%)	2 (2%)	43	62
18	Q	93/93 (100%)	88 (95%)	5 (5%)	20	47
19	R	77/84 (92%)	72 (94%)	5 (6%)	15	42
20	S	78/85 (92%)	75 (96%)	3 (4%)	29	54
21	T	77/78 (99%)	72 (94%)	5 (6%)	15	42
22	U	57/63 (90%)	55 (96%)	2 (4%)	32	56
23	V	67/68 (98%)	64 (96%)	3 (4%)	24	51
24	W	54/55 (98%)	54 (100%)	0	100	100
25	X	48/49 (98%)	46 (96%)	2 (4%)	26	52
26	Y	46/48 (96%)	44 (96%)	2 (4%)	26	51
27	Z	44/49 (90%)	42 (96%)	2 (4%)	24	51
28	AA	38/38 (100%)	38 (100%)	0	100	100
29	AB	51/52 (98%)	47 (92%)	4 (8%)	11	37
30	AC	34/34 (100%)	32 (94%)	2 (6%)	18	44
32	a	171/199 (86%)	168 (98%)	3 (2%)	51	67
33	b	152/190 (80%)	145 (95%)	7 (5%)	24	50
34	c	133/173 (77%)	127 (96%)	6 (4%)	24	51
35	d	117/126 (93%)	115 (98%)	2 (2%)	53	67
36	e	88/116 (76%)	85 (97%)	3 (3%)	32	57
37	f	77/147 (52%)	77 (100%)	0	100	100
38	g	104/105 (99%)	102 (98%)	2 (2%)	50	66
39	h	97/107 (91%)	92 (95%)	5 (5%)	21	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
40	i	80/90 (89%)	78 (98%)	2 (2%)	42	62
41	j	90/99 (91%)	87 (97%)	3 (3%)	33	57
42	k	93/104 (89%)	86 (92%)	7 (8%)	12	38
43	l	90/96 (94%)	88 (98%)	2 (2%)	45	63
44	m	83/84 (99%)	80 (96%)	3 (4%)	31	56
45	n	75/77 (97%)	71 (95%)	4 (5%)	20	47
46	o	65/65 (100%)	63 (97%)	2 (3%)	35	59
47	p	72/78 (92%)	67 (93%)	5 (7%)	14	40
48	q	47/65 (72%)	46 (98%)	1 (2%)	47	64
49	r	70/79 (89%)	66 (94%)	4 (6%)	18	45
50	s	64/66 (97%)	63 (98%)	1 (2%)	55	68
51	t	56/61 (92%)	55 (98%)	1 (2%)	51	67
All	All	4340/4768 (91%)	4173 (96%)	167 (4%)	30	54

5 of 167 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
34	c	85	THR
42	k	118	VAL
34	c	190	LEU
39	h	57	VAL
45	n	69	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
18	Q	31	GLN
47	p	50	ASN
27	Z	18	HIS
46	o	79	ASN
50	s	83	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	119/120 (99%)	33 (27%)	2 (1%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	5	75/76 (98%)	19 (25%)	0
31	2	2831/2903 (97%)	549 (19%)	9 (0%)
52	1	1505/1540 (97%)	303 (20%)	7 (0%)
53	4	42/93 (45%)	9 (21%)	0
All	All	4572/4732 (96%)	913 (19%)	18 (0%)

5 of 913 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	9	G
1	3	12	C
1	3	13	G
1	3	14	U
1	3	15	A

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	1	595	A
52	1	1300	G
52	1	1201	A
31	2	1340	U
52	1	509	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 55 ligands modelled in this entry, 55 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

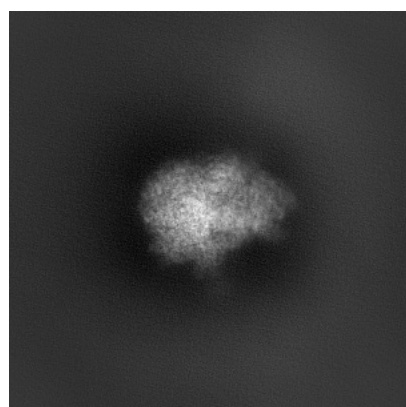
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21422. These allow visual inspection of the internal detail of the map and identification of artifacts.

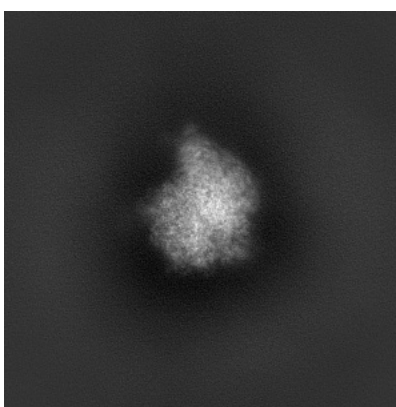
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

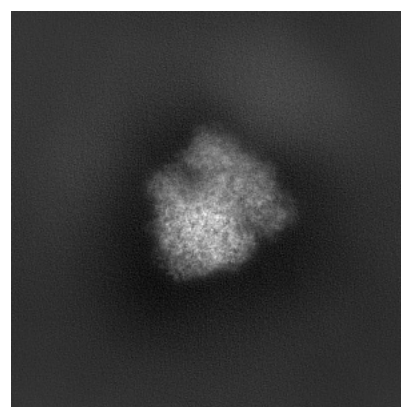
6.1.1 Primary map



X



Y

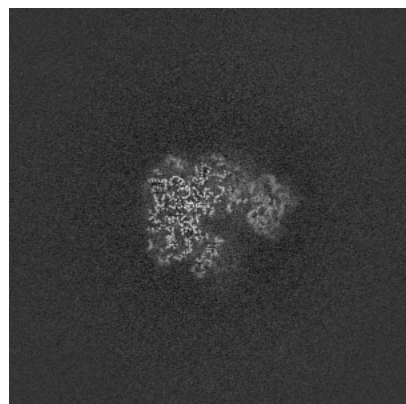


Z

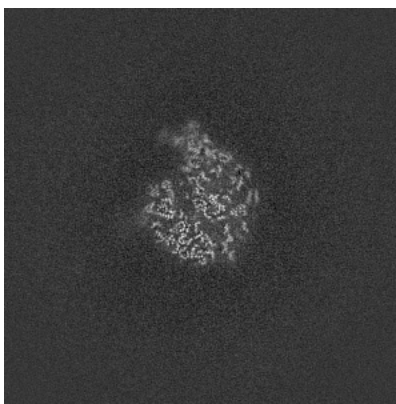
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

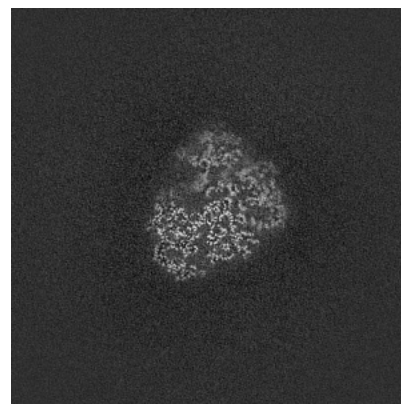
6.2.1 Primary map



X Index: 324



Y Index: 324

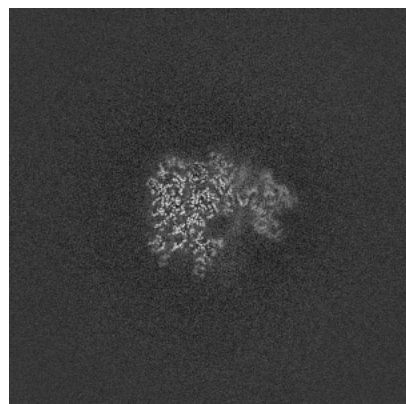


Z Index: 324

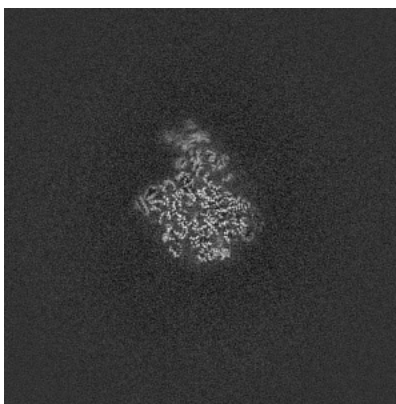
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

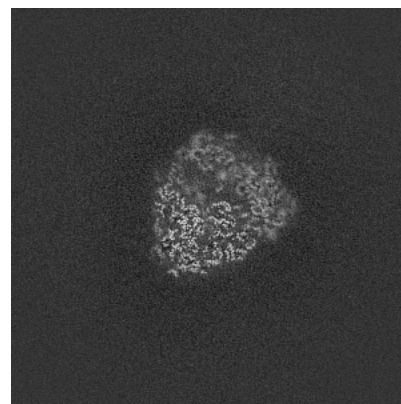
6.3.1 Primary map



X Index: 331



Y Index: 313

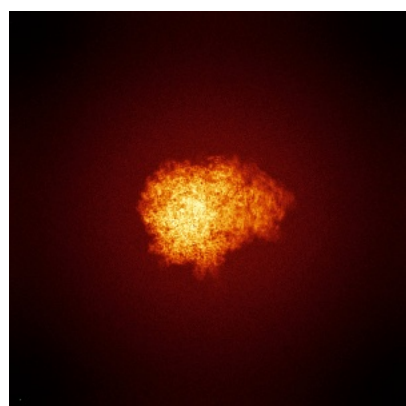


Z Index: 312

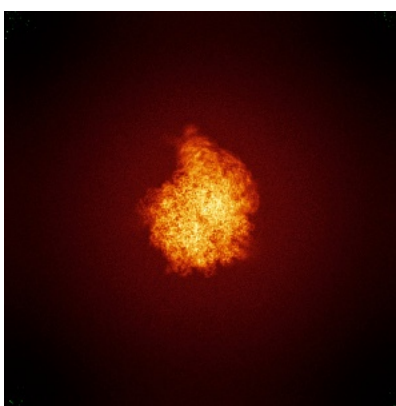
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

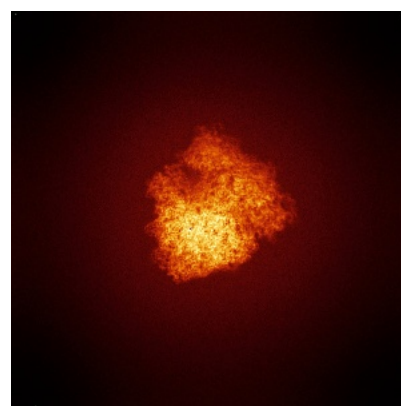
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 5.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

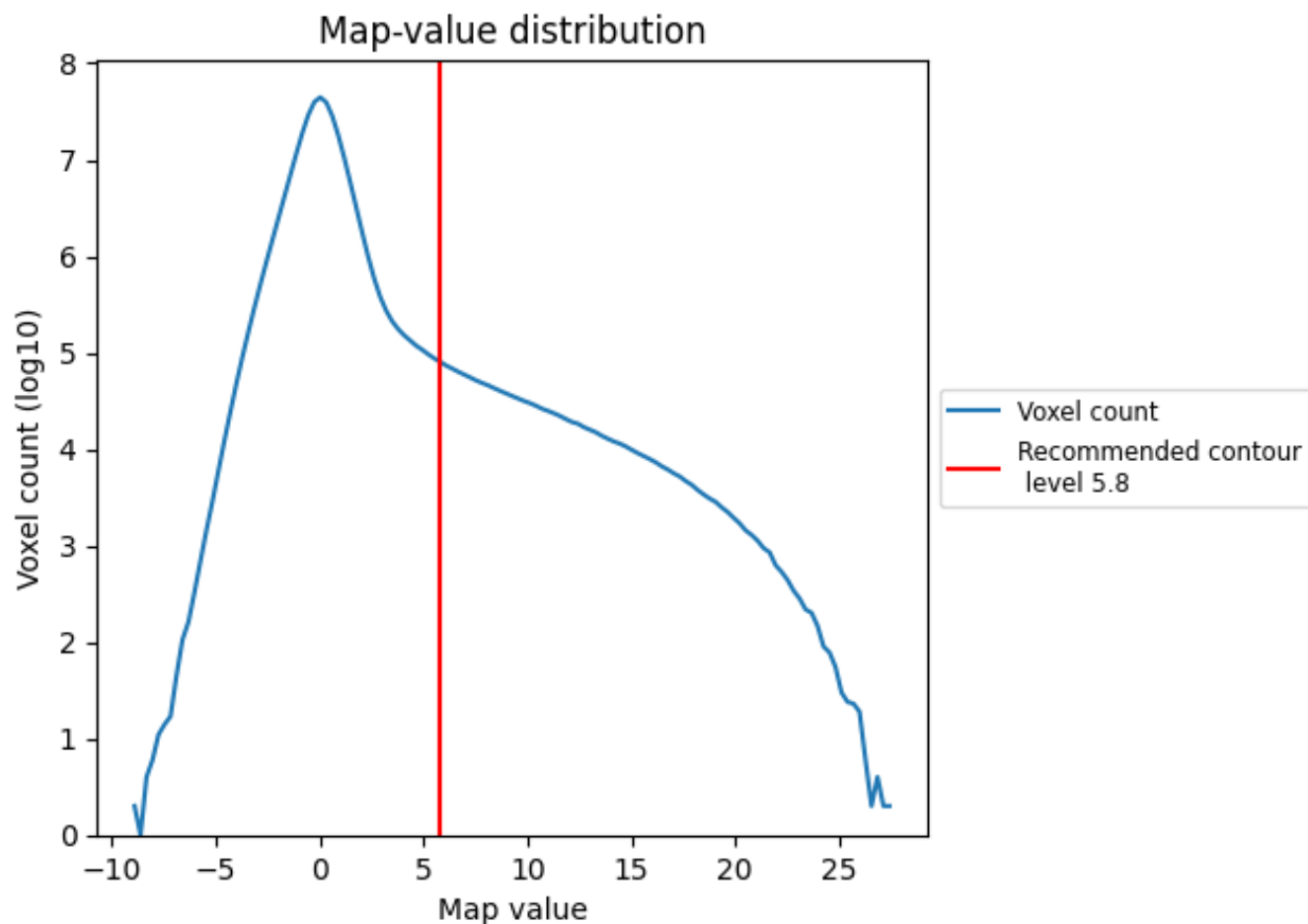
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

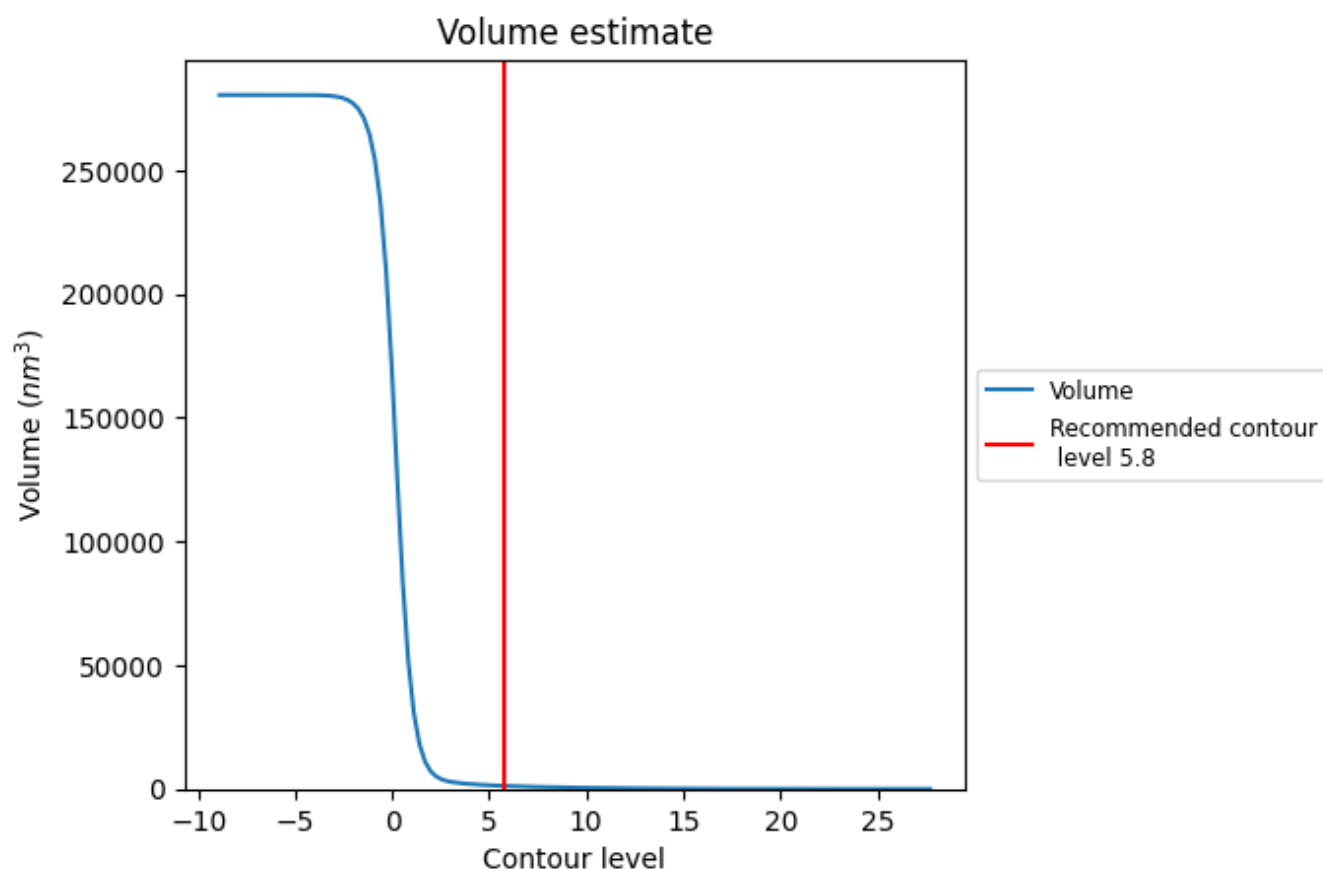
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

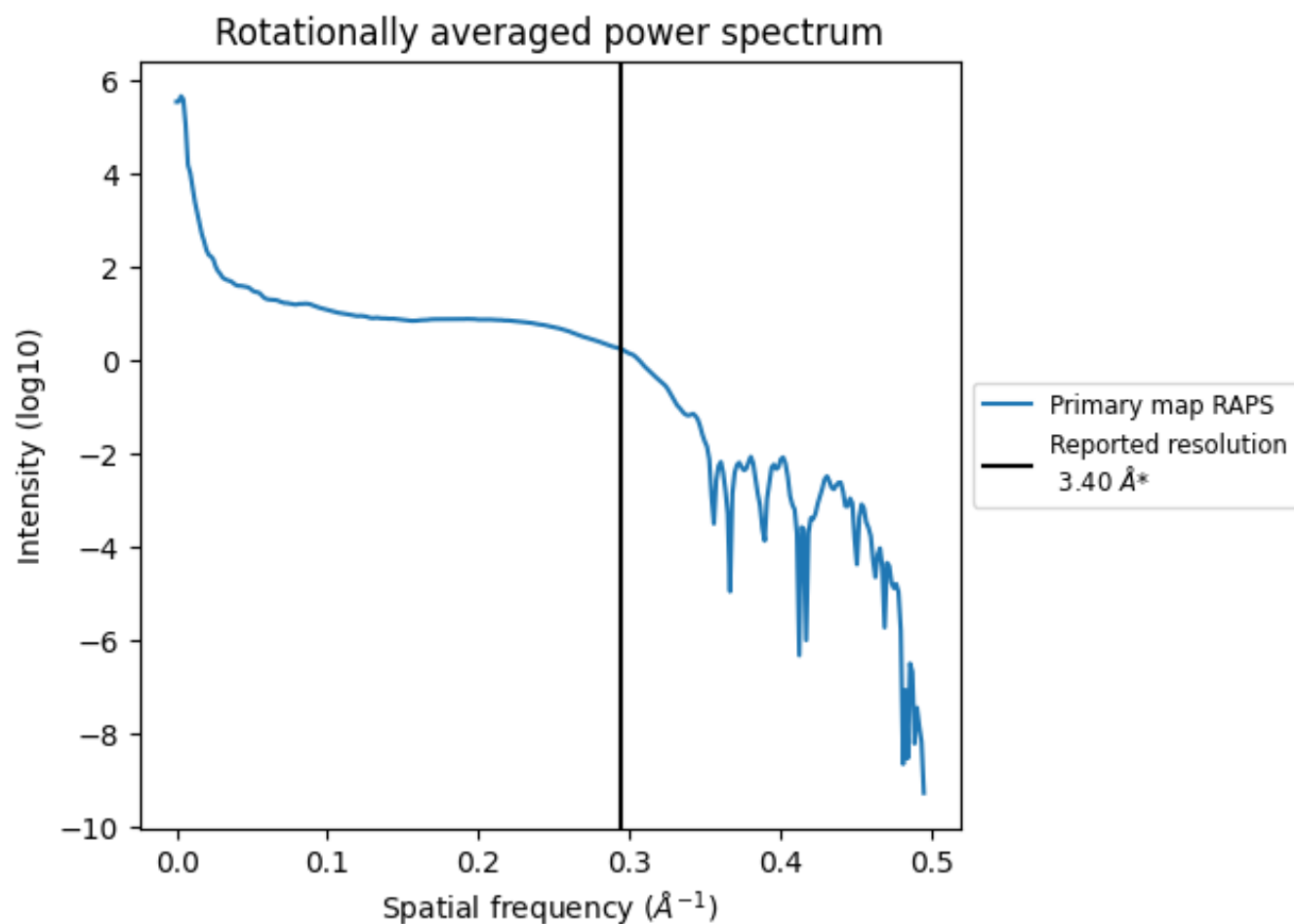
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1233 nm^3 ; this corresponds to an approximate mass of 1114 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

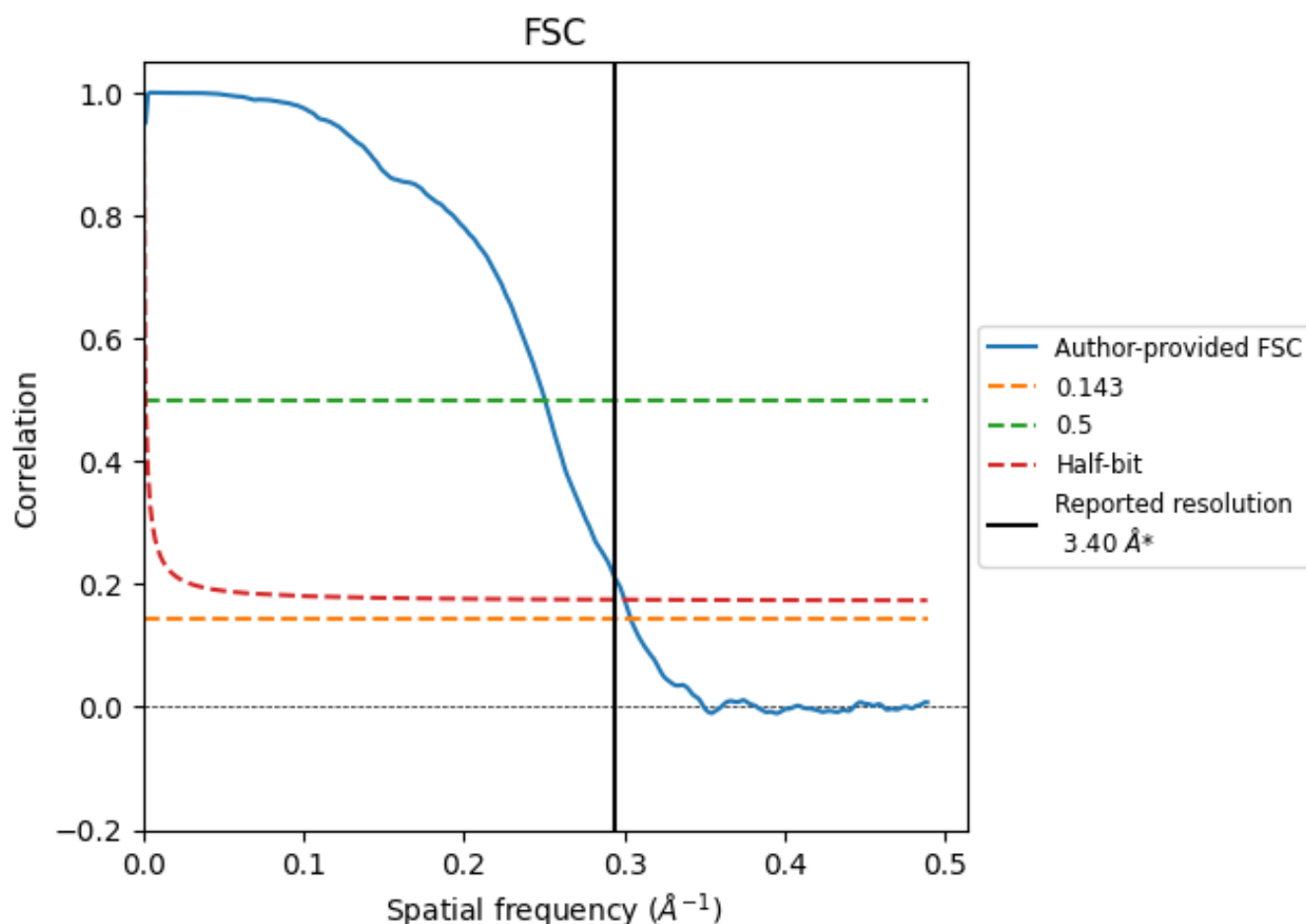


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

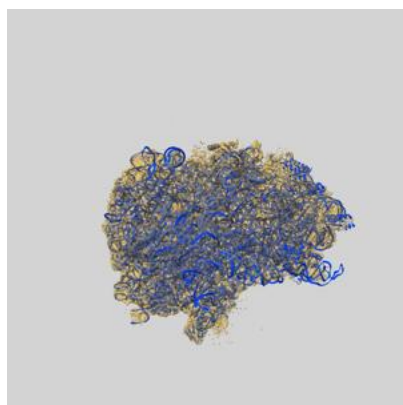
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.29	3.99	3.33
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

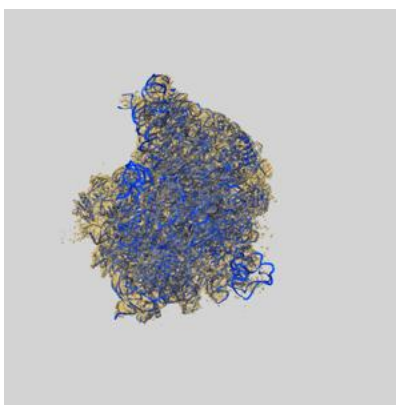
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21422 and PDB model 6VWN. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

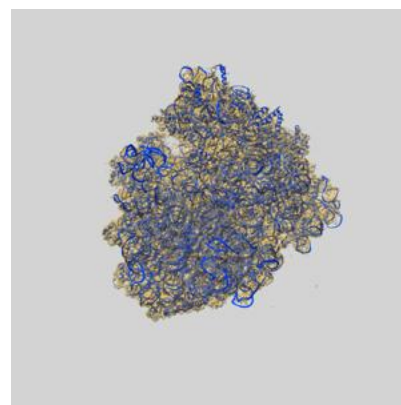
9.1 Map-model overlay [i](#)



X



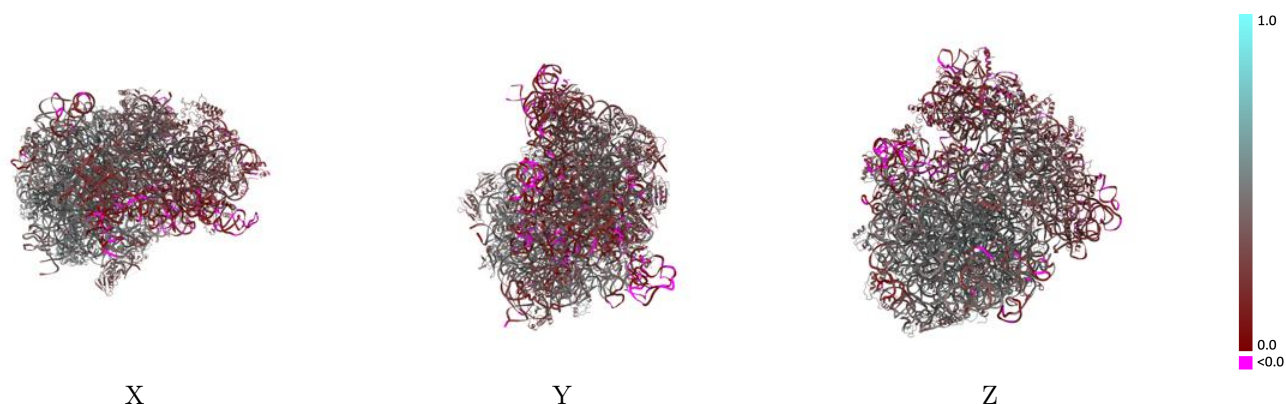
Y



Z

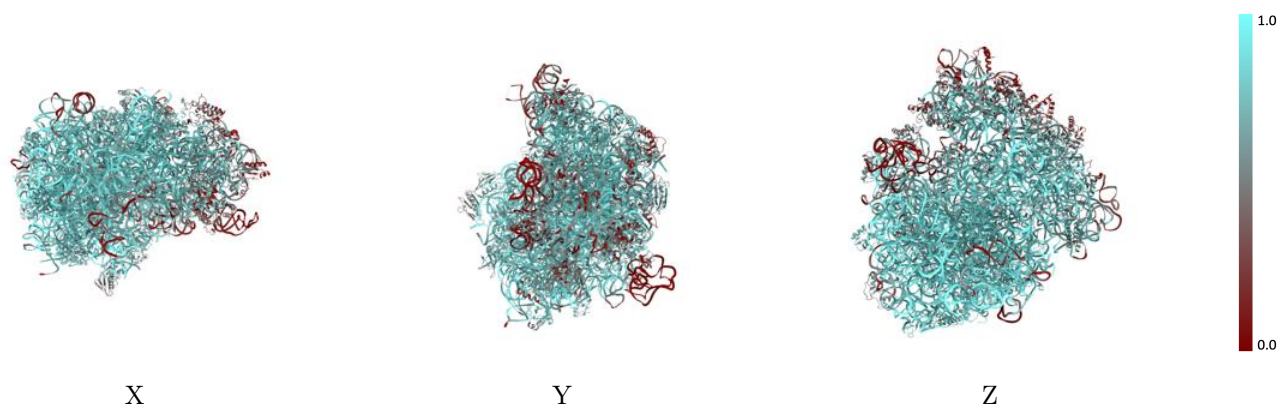
The images above show the 3D surface view of the map at the recommended contour level 5.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



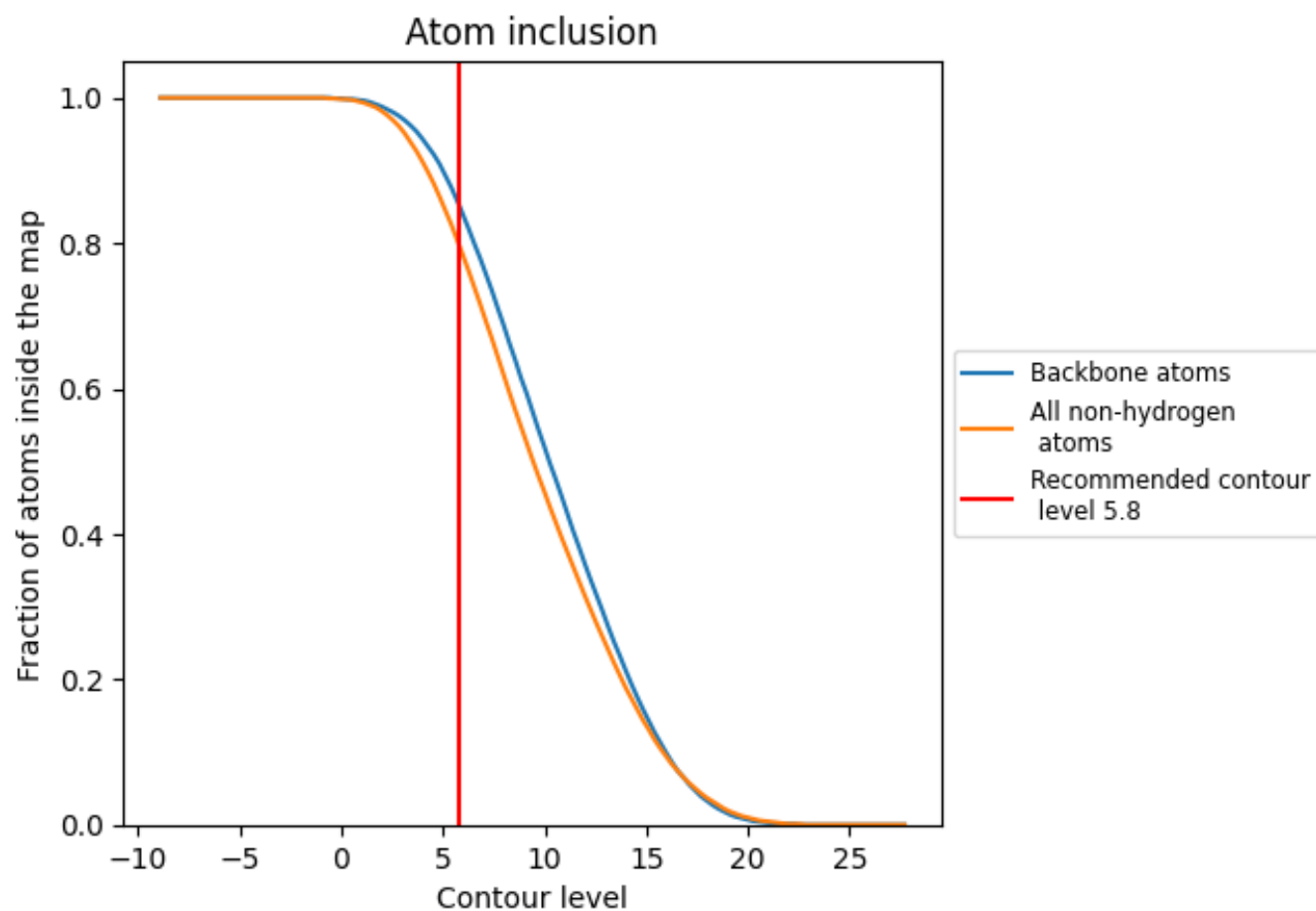
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (5.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (5.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7970	 0.3700
1	 0.7890	 0.2950
2	 0.8900	 0.4250
3	 0.8460	 0.3390
4	 0.3280	 0.0890
5	 0.5920	 0.1470
A	 0.8710	 0.4700
AA	 0.9240	 0.4960
AB	 0.8820	 0.4630
AC	 0.8190	 0.4100
B	 0.8170	 0.4810
C	 0.7680	 0.4510
D	 0.5120	 0.2570
E	 0.6000	 0.3360
F	 0.4850	 0.3540
G	 0.8520	 0.4700
I	 0.8340	 0.4590
J	 0.8100	 0.4660
K	 0.8490	 0.4510
L	 0.8920	 0.4790
M	 0.6870	 0.3540
N	 0.7970	 0.4390
O	 0.8560	 0.4740
P	 0.7830	 0.4680
Q	 0.8330	 0.4740
R	 0.8250	 0.4460
S	 0.7620	 0.4500
T	 0.7180	 0.4150
U	 0.8430	 0.4760
V	 0.8620	 0.4530
W	 0.7410	 0.4100
X	 0.7850	 0.4410
Y	 0.8500	 0.4770
Z	 0.4000	 0.3500
a	 0.3710	 0.2890



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Chain	Atom inclusion	Q-score
b	 0.5570	 0.2940
c	 0.4300	 0.2100
d	 0.7270	 0.3840
e	 0.6510	 0.3420
f	 0.4020	 0.1780
g	 0.7100	 0.3830
h	 0.4030	 0.1840
i	 0.3490	 0.2100
j	 0.6690	 0.3010
k	 0.5920	 0.2600
l	 0.4190	 0.1820
m	 0.5240	 0.2360
n	 0.7070	 0.3540
o	 0.5740	 0.2640
p	 0.6830	 0.3360
q	 0.7350	 0.3520
r	 0.3510	 0.1830
s	 0.6780	 0.2530
t	 0.5070	 0.2400